

O. Nikol

PH#8

1642

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/623,063

DATE: 03/21/2001

TIME: 14:57:04

Input Set : A:\Durrant ('063) Sequence Listing.txt

Output Set: N:\CRF3\03212001\I623063.raw

ENTERED

4 <110> APPLICANT: Durrant, Linda G
5 Spendlove, Ian
6 Hewett, Peter W
7 Ramage, Judith M
9 <120> TITLE OF INVENTION: Anti-angiogenic vaccines: substances and methods
10 relating thereto
12 <130> FILE REFERENCE: 0380-P02286US0
14 <140> CURRENT APPLICATION NUMBER: US 09/623,063
15 <141> CURRENT FILING DATE: 2000-10-24
17 <150> PRIOR APPLICATION NUMBER: PCT/GB99/00583
18 <151> PRIOR FILING DATE: 1999-02-26
20 <150> PRIOR APPLICATION NUMBER: GB 9804121.3
21 <151> PRIOR FILING DATE: 1998-02-26
23 <160> NUMBER OF SEQ ID NOS: 17
25 <170> SOFTWARE: PatentIn Ver. 2.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1124
29 <212> TYPE: PRT
30 <213> ORGANISM: Unknown Organism
32 <220> FEATURE:
33 <223> OTHER INFORMATION: Description of Unknown Organism: Sequence source
34 uncertain
36 <400> SEQUENCE: 1
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40 Ser Gly Thr Val Glu Gly Ala Met Asp Leu Ile Leu Ile Asn Ser Leu
41 20 25 30
43 Pro Leu Val Ser Asp Ala Glu Thr Ser Leu Thr Cys Ile Ala Ser Gly
44 35 40 45
46 Trp Arg Pro His Glu Pro Ile Thr Ile Gly Arg Asp Phe Glu Ala Leu
47 50 55 60
49 Met Asn Gln His Gln Asp Pro Leu Glu Val Thr Gln Asp Val Thr Arg
50 65 70 75 80
52 Glu Trp Ala Lys Lys Val Val Trp Lys Arg Glu Lys Ala Ser Lys Ile
53 85 90 95
55 Asn Gly Ala Tyr Phe Cys Glu Gly Arg Val Arg Gly Glu Ala Ile Arg
56 100 105 110
58 Ile Arg Thr Met Lys Met Arg Gln Gln Ala Ser Phe Leu Pro Ala Thr
59 115 120 125
61 Leu Thr Met Thr Val Asp Lys Gly Asp Asn Val Asn Ile Ser Phe Lys
62 130 135 140
64 Lys Val Leu Ile Lys Glu Glu Asp Ala Val Ile Tyr Lys Asn Gly Ser
65 145 150 155 160
67 Phe Ile His Ser Val Pro Arg His Glu Val Pro Asp Ile Leu Glu Val
68 165 170 175
70 His Leu Pro His Ala Gln Pro Gln Asp Ala Gly Val Tyr Ser Ala Arg
71 180 185 190

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73 Tyr Ile Gly Gly Asn Leu Phe Thr Ser Ala Phe Thr Arg Leu Ile Val
74      195      200      205
76 Arg Arg Cys Glu Ala Gln Lys Trp Gly Pro Glu Cys Asn His Leu Cys
77      210      215      220
79 Thr Ala Cys Met Asn Asn Gly Val Cys His Glu Asp Thr Gly Glu Cys
80 225      230      235      240
82 Ile Cys Pro Pro Gly Phe Met Gly Arg Thr Cys Glu Lys Ala Cys Glu
83      245      250      255
85 Leu His Thr Phe Gly Arg Thr Cys Lys Glu Arg Cys Ser Gly Gln Glu
86      260      265      270
88 Gly Cys Lys Ser Tyr Val Phe Cys Leu Pro Asp Pro Tyr Gly Cys Ser
89      275      280      285
91 Cys Ala Thr Gly Trp Lys Gly Leu Gln Cys Asn Glu Ala Cys His Pro
92      290      295      300
94 Gly Phe Tyr Gly Pro Asp Cys Lys Leu Arg Cys Ser Cys Asn Asn Gly
95 305      310      315      320
97 Glu Met Cys Asp Arg Phe Gln Gly Cys Leu Cys Ser Pro Gly Trp Gln
98      325      330      335
100 Gly Leu Gln Cys Glu Arg Glu Gly Ile Pro Arg Met Thr Pro Lys Ile
101      340      345      350
103 Val Asp Leu Pro Asp His Ile Glu Val Asn Ser Gly Lys Phe Asn Pro
104      355      360      365
106 Ile Cys Lys Ala Ser Gly Trp Pro Leu Pro Thr Asn Glu Glu Met Thr
107      370      375      380
109 Leu Val Lys Pro Asp Gly Thr Val Leu His Pro Lys Asp Phe Asn His
110 385      390      395      400
112 Thr Asp His Phe Ser Val Ala Ile Phe Thr Ile His Arg Ile Leu Pro
113      405      410      415
115 Pro Asp Ser Gly Val Trp Val Cys Ser Val Asn Thr Val Ala Gly Met
116      420      425      430
118 Val Glu Lys Pro Phe Asn Ile Ser Val Lys Val Leu Pro Lys Pro Leu
119      435      440      445
121 Asn Ala Pro Asn Val Ile Asp Thr Gly His Asn Phe Ala Val Ile Asn
122      450      455      460
124 Ile Ser Ser Glu Pro Tyr Phe Gly Asp Gly Pro Ile Lys Ser Lys Lys
125 465      470      475      480
127 Leu Leu Tyr Lys Pro Val Asn His Tyr Glu Ala Trp Gln His Ile Gln
128      485      490      495
130 Val Thr Asn Glu Ile Val Thr Leu Asn Tyr Leu Glu Pro Arg Thr Glu
131      500      505      510
133 Tyr Glu Leu Cys Val Gln Leu Val Arg Arg Gly Glu Gly Gly Glu Gly
134      515      520      525
136 His Pro Gly Pro Val Arg Arg Phe Thr Thr Ala Ser Ile Gly Leu Pro
137      530      535      540
139 Pro Pro Arg Gly Leu Asn Leu Leu Pro Lys Ser Gln Thr Thr Leu Asn
140 545      550      555      560
142 Leu Thr Trp Gln Pro Ile Phe Pro Ser Ser Glu Asp Asp Phe Tyr Val
143      565      570      575
145 Glu Val Glu Arg Arg Ser Val Gln Lys Ser Asp Gln Gln Asn Ile Lys

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146          580          585          590
148 Val Pro Gly Asn Leu Thr Ser Val Leu Leu Asn Asn Leu His Pro Arg
149          595          600          605
151 Glu Gln Tyr Val Val Arg Ala Arg Val Asn Thr Lys Ala Gln Gly Glu
152          610          615          620
154 Trp Ser Glu Asp Leu Thr Ala Trp Thr Leu Ser Asp Ile Leu Pro Pro
155 625          630          635          640
157 Gln Pro Glu Asn Ile Lys Ile Ser Asn Ile Thr His Ser Ser Ala Val
158          645          650          655
160 Ile Ser Trp Thr Ile Leu Asp Gly Tyr Ser Ile Ser Ser Ile Thr Ile
161          660          665          670
163 Arg Tyr Lys Val Gln Gly Lys Asn Glu Asp Gln His Val Asp Val Lys
164          675          680          685
166 Ile Lys Asn Ala Thr Ile Ile Gln Tyr Gln Leu Lys Gly Leu Glu Pro
167          690          695          700
169 Glu Thr Ala Tyr Gln Val Asp Ile Phe Ala Glu Asn Asn Ile Gly Ser
170 705          710          715          720
172 Ser Asn Pro Ala Phe Ser His Glu Leu Val Thr Leu Pro Glu Ser Gln
173          725          730          735
175 Ala Pro Ala Asp Leu Gly Gly Gly Lys Met Leu Leu Ile Ala Ile Leu
176          740          745          750
178 Gly Ser Ala Gly Met Thr Cys Leu Thr Val Leu Leu Ala Phe Leu Ile
179          755          760          765
181 Ile Leu Gln Leu Lys Arg Ala Asn Val Gln Arg Arg Met Ala Gln Ala
182          770          775          780
184 Phe Gln Asn Val Arg Glu Glu Pro Ala Val Gln Phe Asn Ser Gly Thr
185 785          790          795          800
187 Leu Ala Leu Asn Arg Lys Val Lys Asn Asn Pro Asp Pro Thr Ile Tyr
188          805          810          815
190 Pro Val Leu Asp Trp Asn Asp Ile Lys Phe Gln Asp Val Ile Gly Glu
191          820          825          830
193 Gly Asn Phe Gly Gln Val Leu Lys Ala Arg Ile Lys Lys Asp Gly Leu
194          835          840          845
196 Arg Met Asp Ala Ala Ile Lys Arg Met Lys Glu Tyr Ala Ser Lys Asp
197          850          855          860
199 Asp His Arg Asp Phe Ala Gly Glu Leu Glu Val Leu Cys Lys Leu Gly
200 865          870          875          880
202 His His Pro Asn Ile Ile Asn Leu Leu Gly Ala Cys Glu His Arg Gly
203          885          890          895
205 Tyr Leu Tyr Leu Ala Ile Glu Tyr Ala Pro His Gly Asn Leu Leu Asp
206          900          905          910
208 Phe Leu Arg Lys Ser Arg Val Leu Glu Thr Asp Pro Ala Phe Ala Ile
209          915          920          925
211 Ala Asn Ser Thr Ala Ser Thr Leu Ser Ser Gln Gln Leu Leu His Phe
212          930          935          940
214 Ala Ala Asp Val Ala Arg Gly Met Asp Tyr Leu Ser Gln Lys Gln Phe
215 945          950          955          960
217 Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Gly Glu Asn Tyr
218          965          970          975

```

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```

220 Val Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Gly Gln Glu Val Tyr
221          980          985          990
223 Val Lys Lys Thr Met Gly Arg Leu Pro Val Arg Trp Met Ala Ile Glu
224          995          1000          1005
226 Ser Leu Asn Tyr Ser Val Tyr Thr Thr Asn Ser Asp Val Trp Ser Tyr
227        1010          1015          1020
229 Gly Val Leu Leu Trp Glu Ile Val Ser Leu Gly Gly Thr Pro Tyr Cys
230      1025          1030          1035          1040
232 Gly Met Thr Cys Ala Glu Leu Tyr Glu Lys Leu Pro Gln Gly Tyr Arg
233          1045          1050          1055
235 Leu Glu Lys Pro Leu Asn Cys Asp Asp Glu Val Tyr Asp Leu Met Arg
236          1060          1065          1070
238 Gln Cys Trp Arg Glu Lys Pro Tyr Glu Arg Pro Ser Phe Ala Gln Ile
239          1075          1080          1085
241 Leu Val Ser Leu Asn Arg Met Leu Glu Glu Arg Lys Thr Tyr Val Asn
242        1090          1095          1100
244 Thr Thr Leu Tyr Glu Lys Phe Thr Tyr Ala Gly Ile Asp Cys Ser Ala
245      1105          1110          1115          1120
247 Glu Glu Ala Ala
253 <210> SEQ ID NO: 2
254 <211> LENGTH: 1138
255 <212> TYPE: PRT
256 <213> ORGANISM: Unknown Organism
258 <220> FEATURE:
259 <223> OTHER INFORMATION: Description of Unknown Organism: Sequence source
260      uncertain
262 <400> SEQUENCE: 2
263 Met Val Trp Arg Val Pro Pro Phe Leu Leu Pro Ile Leu Phe Leu Ala
264    1          5          10          15
266 Ser His Val Gly Ala Ala Val Asp Leu Thr Leu Leu Ala Asn Leu Arg
267          20          25          30
269 Leu Thr Asp Pro Gln Arg Phe Phe Leu Thr Cys Val Ser Gly Glu Ala
270          35          40          45
272 Gly Ala Gly Arg Gly Ser Asp Ala Trp Gly Pro Pro Leu Leu Leu Glu
273          50          55          60
275 Lys Asp Asp Arg Ile Val Arg Thr Pro Pro Gly Pro Pro Leu Arg Leu
276        65          70          75          80
278 Ala Arg Asn Gly Ser His Gln Val Thr Leu Arg Gly Phe Ser Lys Pro
279          85          90          95
281 Ser Asp Leu Val Gly Val Phe Ser Cys Val Gly Gly Ala Gly Ala Arg
282          100          105          110
284 Arg Thr Arg Val Ile Tyr Val His Asn Ser Pro Gly Ala His Leu Leu
285          115          120          125
287 Pro Asp Lys Val Thr His Thr Val Asn Lys Gly Asp Thr Ala Val Leu
288          130          135          140
290 Ser Ala Arg Val His Lys Glu Lys Gln Thr Asp Val Ile Trp Lys Ser
291      145          150          155          160
293 Asn Gly Ser Tyr Phe Tyr Thr Leu Asp Trp His Glu Ala Gln Asp Gly
294          165          170          175

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```

296 Arg Phe Leu Leu Gln Leu Pro Asn Val Gln Pro Pro Ser Ser Gly Ile
297      180      185      190
299 Tyr Ser Ala Thr Tyr Leu Glu Ala Ser Pro Leu Gly Ser Ala Phe Phe
300      195      200      205
302 Arg Leu Ile Val Arg Gly Cys Gly Ala Gly Arg Trp Gly Pro Gly Cys
303      210      215      220
305 Thr Lys Glu Cys Pro Gly Cys Leu His Gly Gly Val Cys His Asp His
306 225      230      235      240
308 Asp Gly Glu Cys Val Cys Pro Pro Gly Phe Thr Gly Thr Arg Cys Glu
309      245      250      255
311 Gln Ala Cys Arg Glu Gly Arg Phe Gly Gln Ser Cys Gln Glu Gln Cys
312      260      265      270
314 Pro Gly Ile Ser Gly Cys Arg Gly Leu Thr Phe Cys Leu Pro Asp Pro
315      275      280      285
317 Tyr Gly Cys Ser Cys Gly Ser Gly Trp Arg Gly Ser Gln Cys Gln Glu
318      290      295      300
320 Ala Cys Ala Pro Gly His Phe Gly Ala Asp Cys Arg Leu Gln Cys Gln
321 305      310      315      320
323 Cys Gln Asn Gly Gly Thr Cys Asp Arg Phe Ser Gly Cys Val Cys Pro
324      325      330      335
326 Ser Gly Trp His Gly Val His Cys Glu Lys Ser Asp Arg Ile Pro Gln
327      340      345      350
329 Ile Leu Asn Met Ala Ser Glu Leu Glu Phe Asn Leu Glu Thr Met Pro
330      355      360      365
332 Arg Ile Asn Cys Ala Ala Ala Gly Asn Pro Phe Pro Val Arg Gly Ser
333      370      375      380
335 Ile Glu Leu Arg Lys Pro Asp Gly Thr Val Leu Leu Ser Thr Lys Ala
336 385      390      395      400
338 Ile Val Glu Pro Glu Lys Thr Thr Ala Glu Phe Glu Val Pro Arg Leu
339      405      410      415
341 Val Leu Ala Asp Ser Gly Phe Trp Glu Cys Arg Val Ser Thr Ser Gly
342      420      425      430
344 Gly Gln Asp Ser Arg Arg Phe Lys Val Asn Val Lys Val Pro Pro Val
345      435      440      445
347 Pro Leu Ala Ala Pro Arg Leu Leu Thr Lys Gln Ser Arg Gln Leu Val
348      450      455      460
350 Val Ser Pro Leu Val Ser Phe Ser Gly Asp Gly Pro Ile Ser Thr Val
351 465      470      475      480
353 Arg Leu His Tyr Arg Pro Gln Asp Ser Thr Met Asp Trp Ser Thr Ile
354      485      490      495
356 Val Val Asp Pro Ser Glu Asn Val Thr Leu Met Asn Leu Arg Pro Lys
357      500      505      510
359 Thr Gly Tyr Ser Val Arg Val Gln Leu Ser Arg Pro Gly Glu Gly Gly
360      515      520      525
362 Glu Gly Ala Trp Gly Pro Pro Thr Leu Met Thr Thr Asp Cys Pro Glu
363      530      535      540
365 Pro Leu Leu Gln Pro Trp Leu Glu Gly Trp His Val Glu Gly Thr Asp
366 545      550      555      560
368 Arg Leu Arg Val Ser Trp Ser Leu Pro Leu Val Pro Gly Pro Leu Val

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VERIFICATION SUMMARY

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